CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

University of Kansas

Lawrence KS

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Characterization of Potter and Polka14, two mycobacteriophages isolated from soil samples in Lawrence, Kansas

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Mycobacterium smegmatis is a common soil bacterium that is a non-pathogenic close relative of Mycobacterium tuberculosis, the causative agent in Tuberculosis. One laboratory section of the introductory biology course at the University of Kansas took part in an Howard Hughes Medical Institute-sponsored project to isolate and characterized bacteriophages that can infect M. smeg. Fifteen unique phages were isolated from soil samples collected throughout Lawrence, Kansas, purified to high concentration, and examined by electron microscopy and DNA fingerprinting. Genomic DNA from two selected bacteriophages was subjected to whole genome sequencing at the University of Pittsburgh. Phage Potter is a lytic phage that was found near Potter lake on the KU campus. Its genome sequence indicates that it belongs to subcluster B1 mycobacteriophages. Polka14 is a lytic phage producing very small plaques that clusters with F1 mycobacteriophages. During the annotation of Potter, we discovered that within B1 phages, gp10 comes in two forms, either an 87 amino acid protein or a 45 amino acid protein that results from a mutated start codon in the shorter protein phages. We are exploring the evolution of gp 10 in B1 phages, and are attempting to express the longer and shorter products in bacteria so that we can isolate and begin biochemical characterization of the proteins. To gain a better appreciation of the diversity in the samples collected by the class, we are using the Phage Enzyme Tool (PET) to estimate the cluster and subcluster of each sample and are comparing these results with a method using polymerase chain reaction of tape measure genes to predict cluster assignment. Together these results will contribute to a better understanding of the diversity of mycobactriophages, and may provide insights into the structure and function of viral proteins that can potentially be useful in understanding the viral life cycle and its interaction with host bacteria.